Figure 1

Spacing Between Adjacent Peaks in the Raw Data
(M13, T's T=6%, 60C, Long Gel)
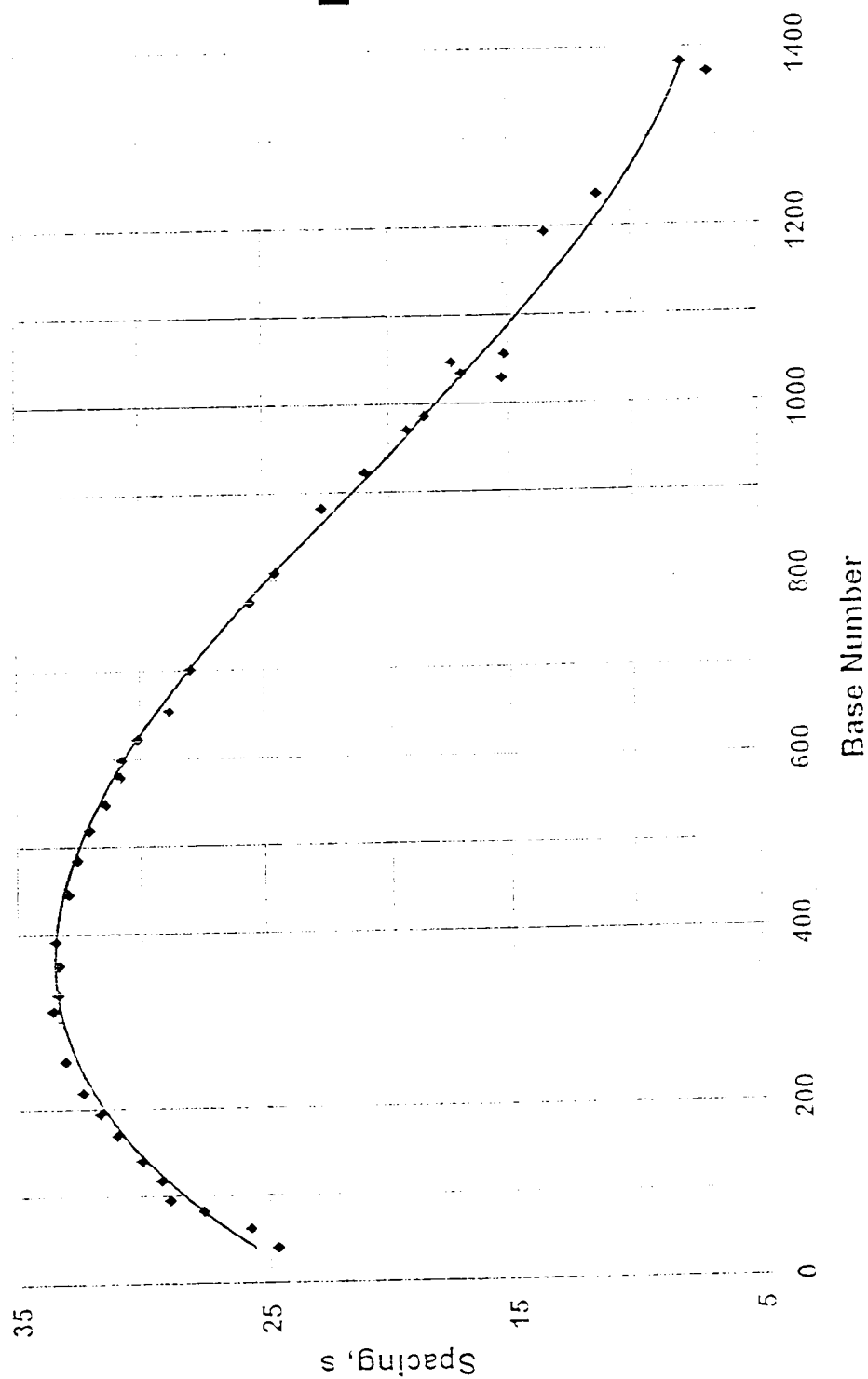
Spacing Between Adjacent Bases
(for Different Number of Peaks Used for Alignment of Raw Data)
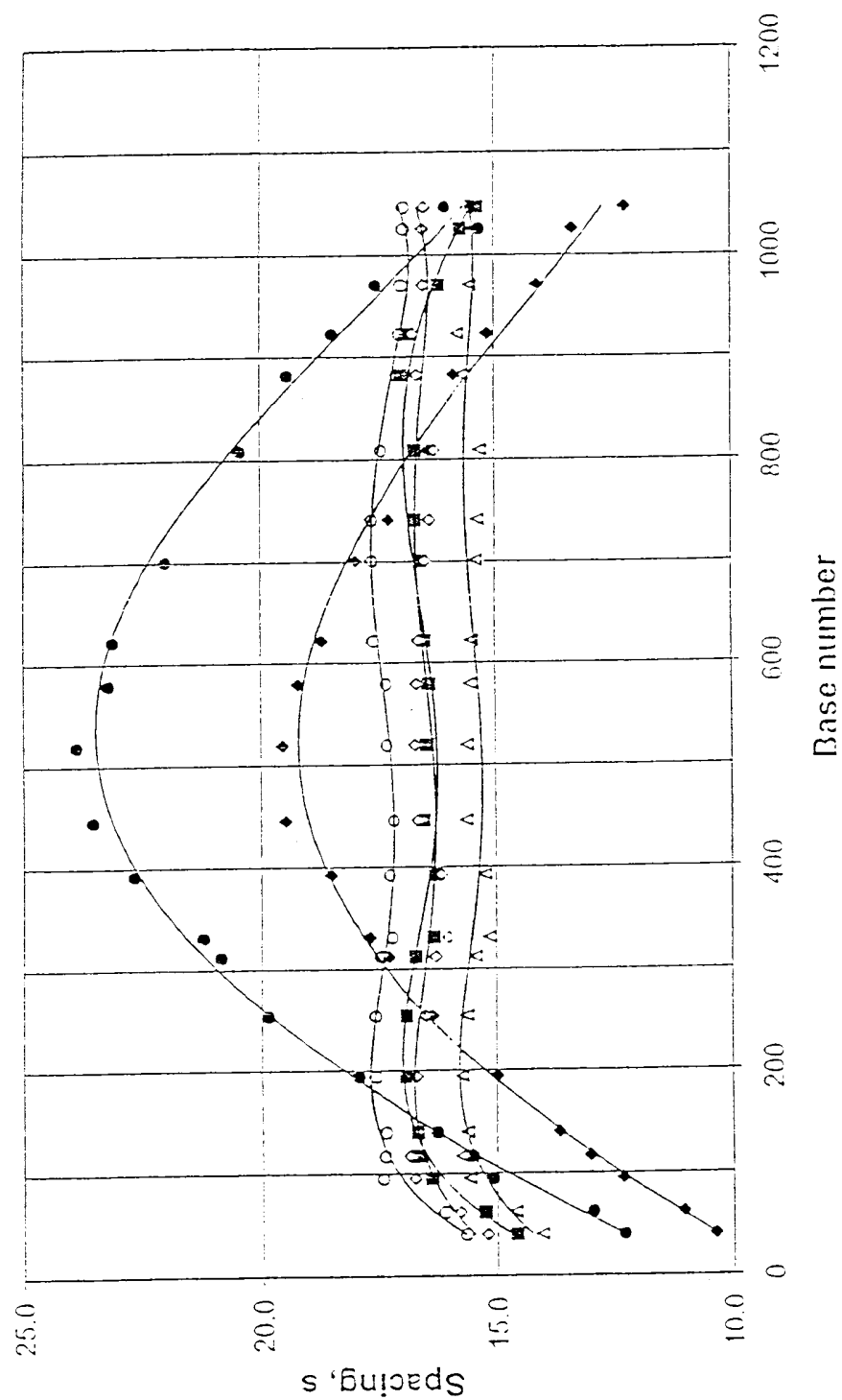(M13, Long Gel, 55C, T=6%)

Figure 2

Standard Deviation (%) of the Spacing Between Adjacent Bases from Average as a Function of Number of Peaks Used as a Reference for Alignment of Raw Data

St. Deviation, %
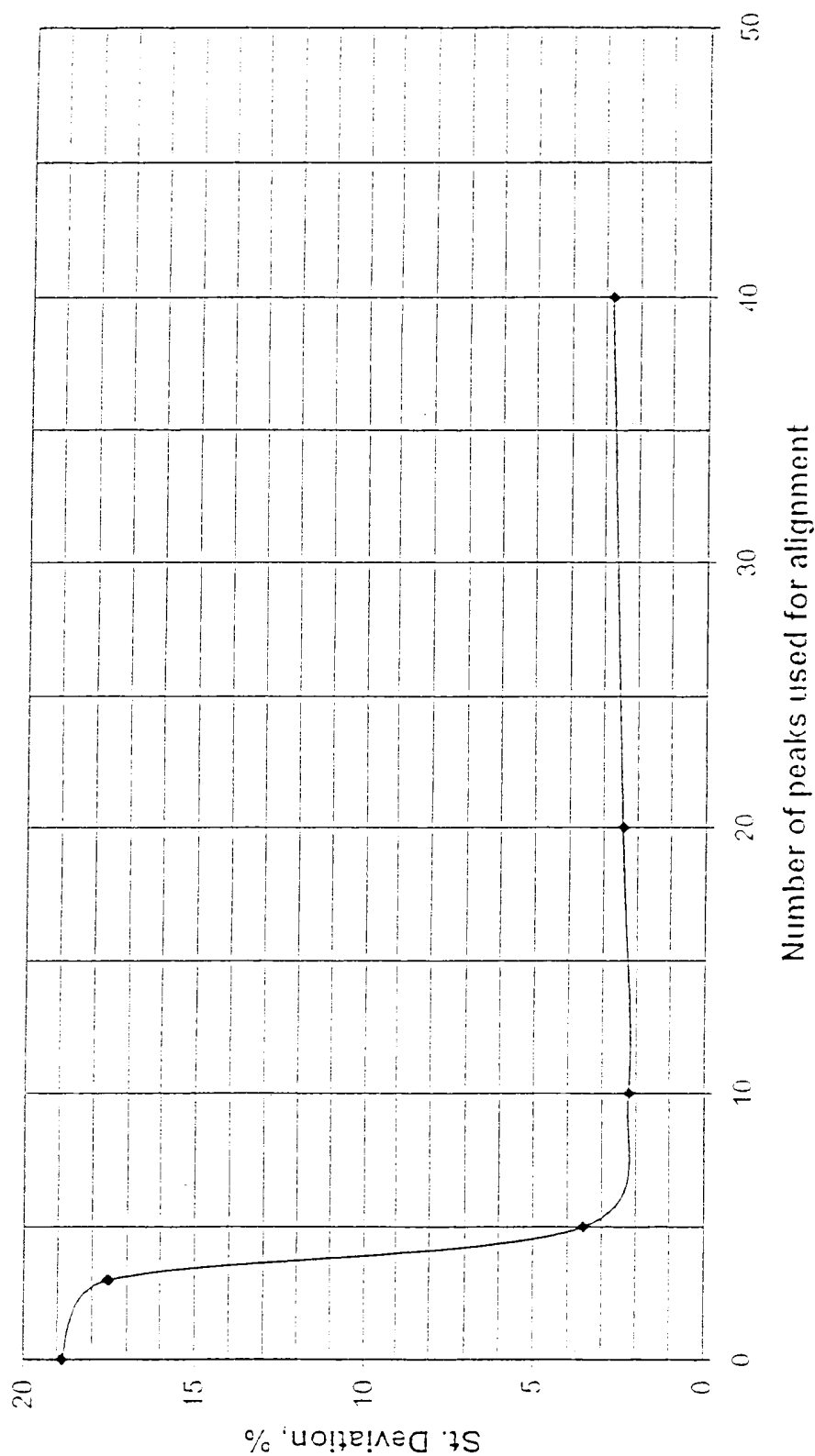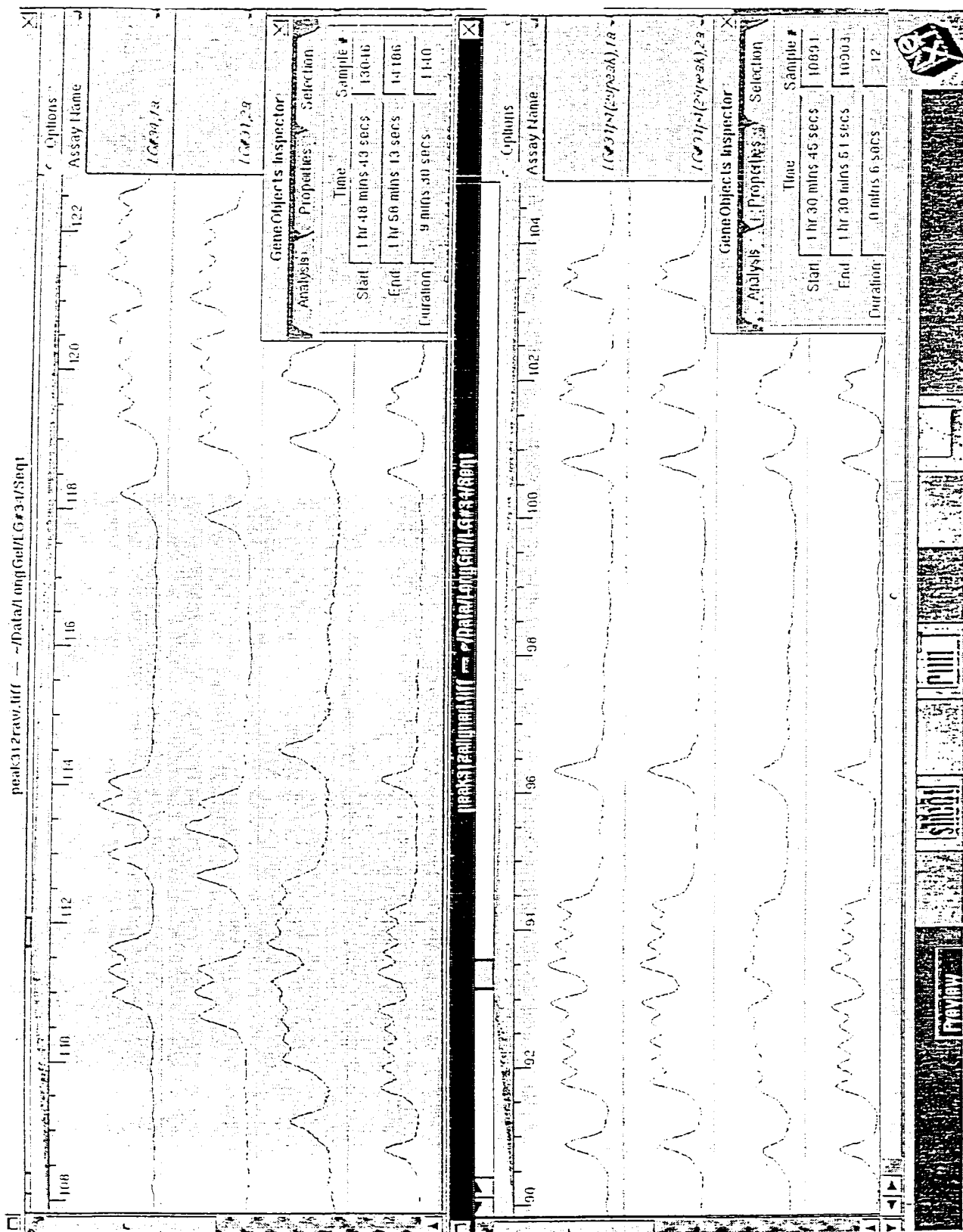
Number of peaks used for alignment

Figure 3

Figure 4

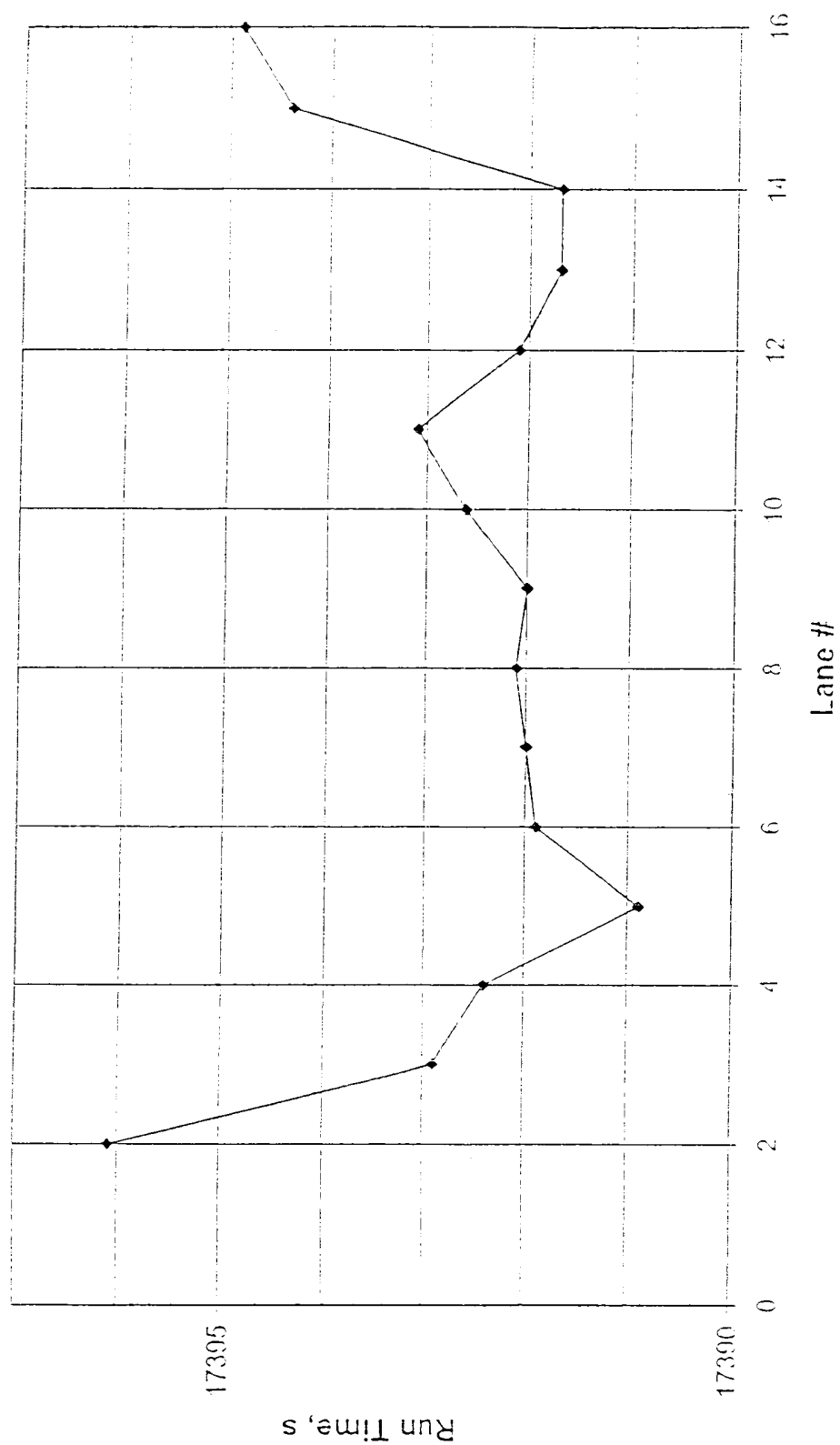Run Time of the BP#1056 in Different Lanes
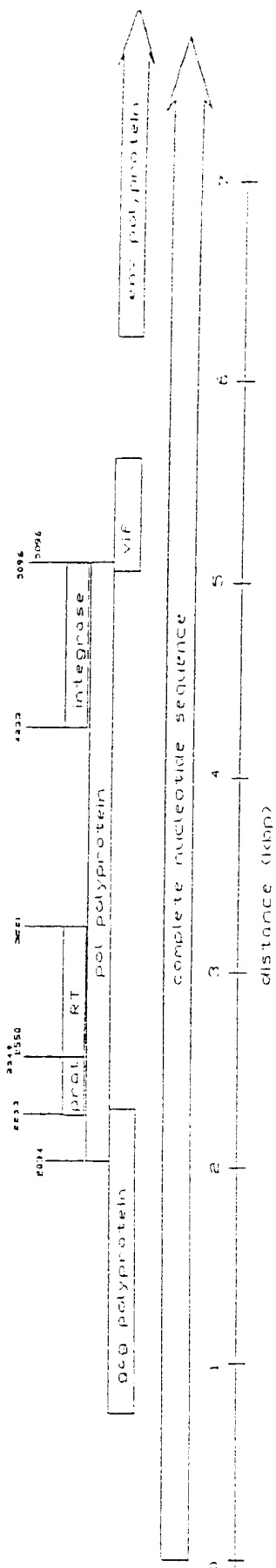(after alignment based on 10 peaks)

Figure 5

RT-PCR amplicon (1.3 kbp)

gag polyprotein

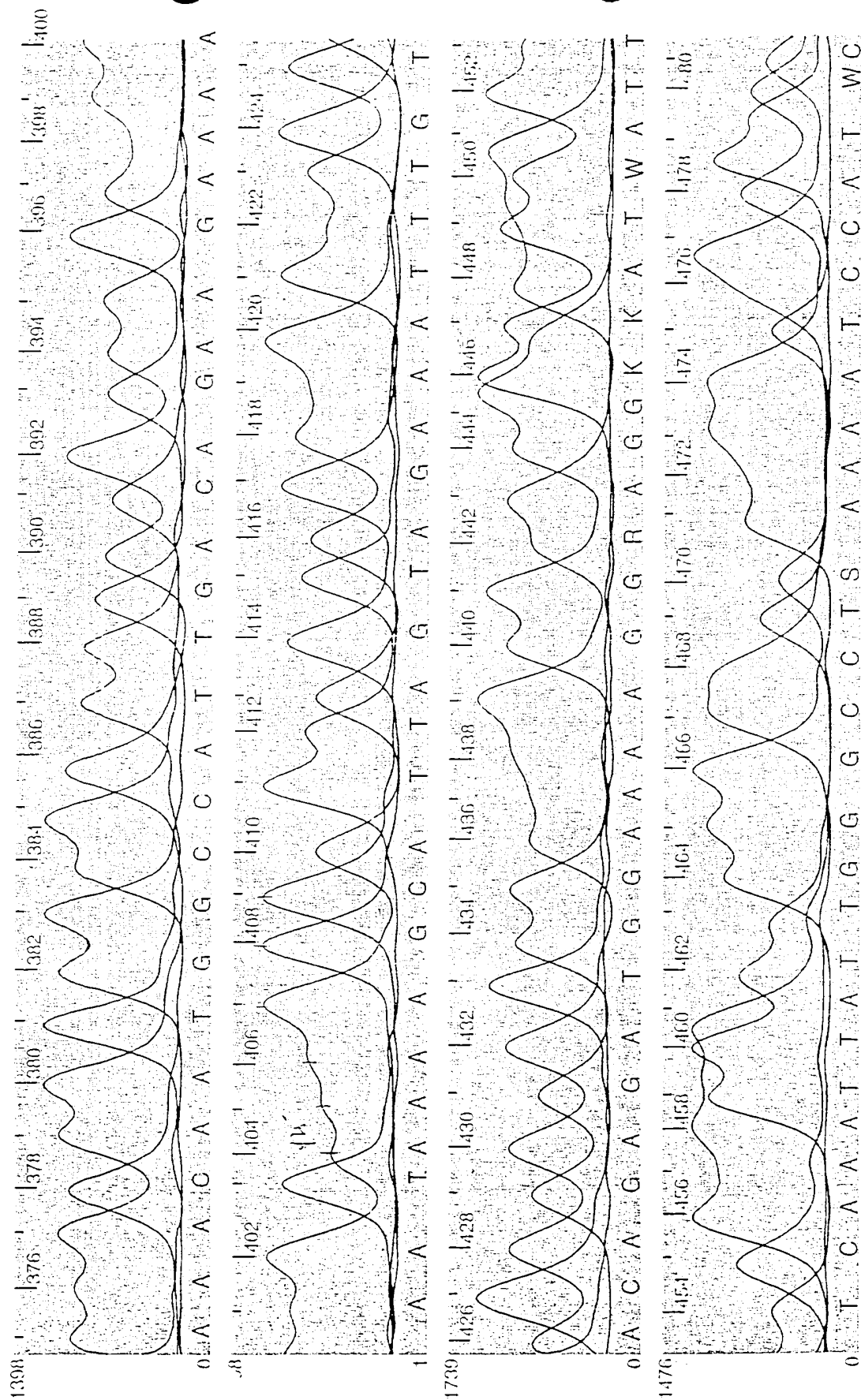pol polyprotein

prot

RT

integrase

vif

complete nucleotide sequence

enc pol protein

distance (kbp)

Figure 6

Figure 7
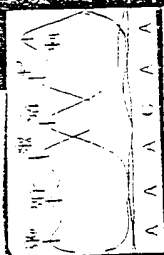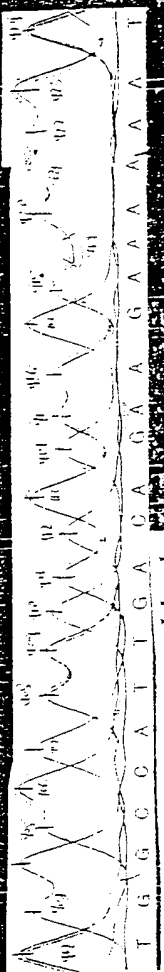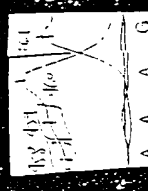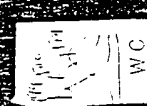
Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

Figure 8

Figure 9A

Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

Figure 9B

Figure 9C

Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc
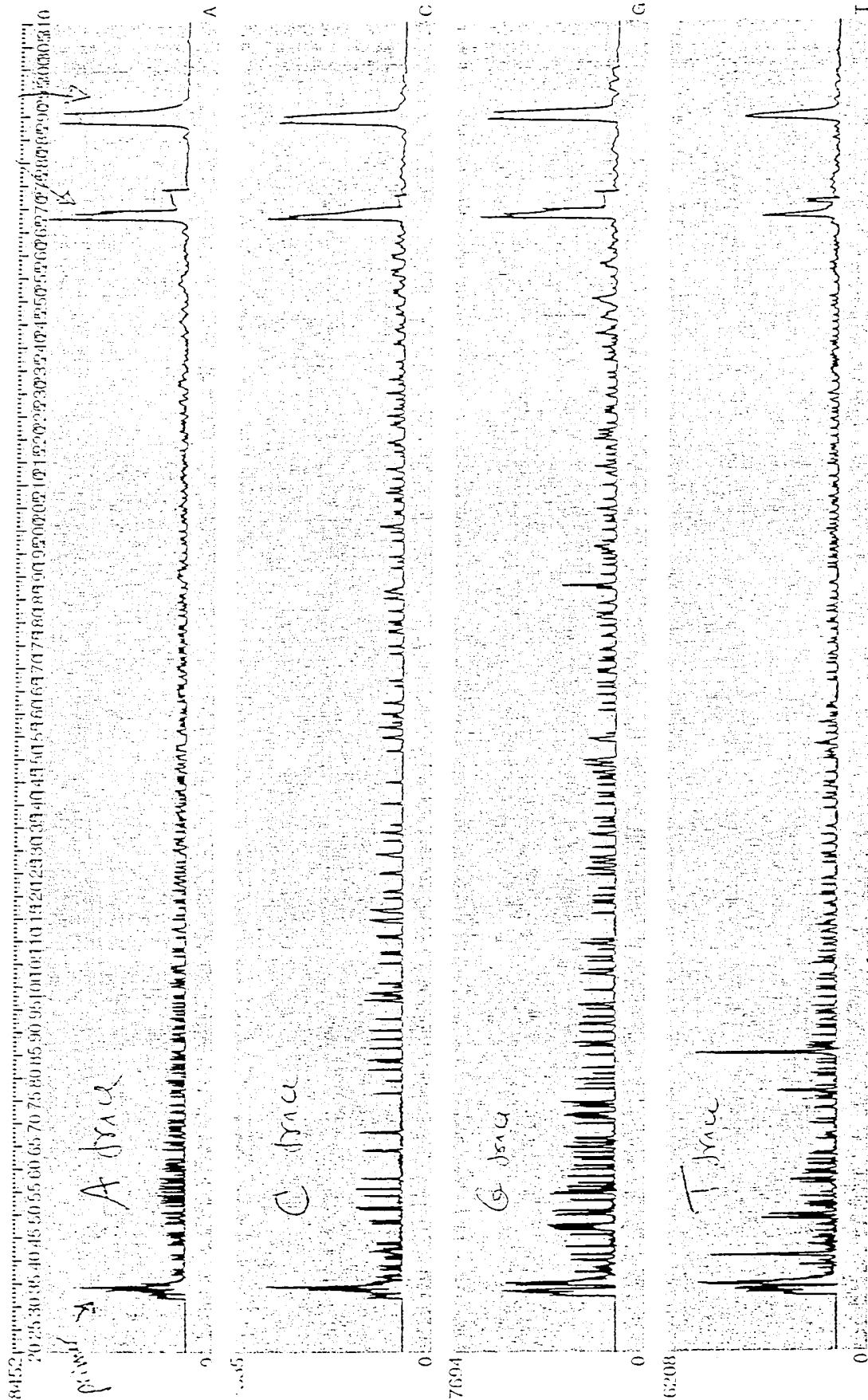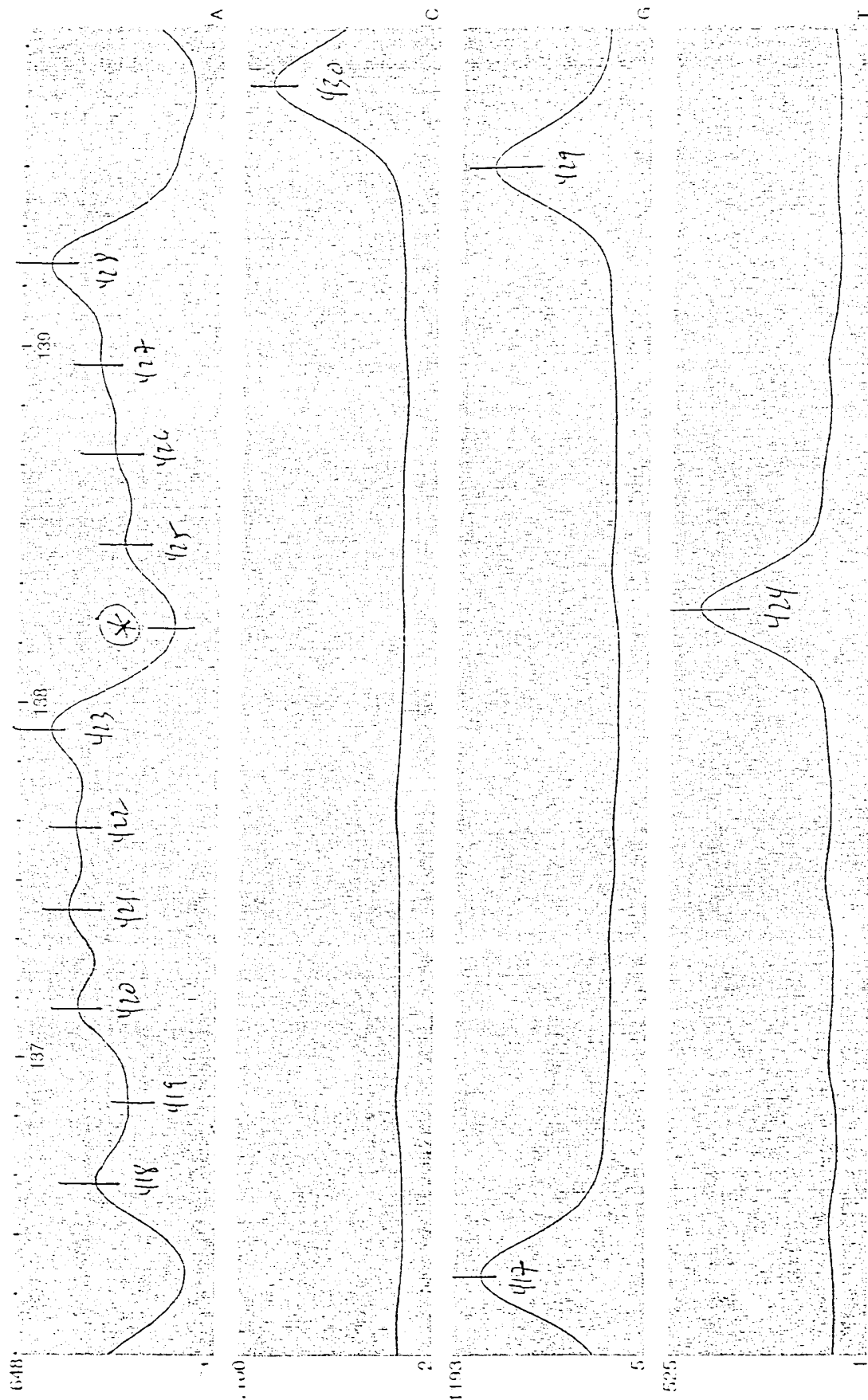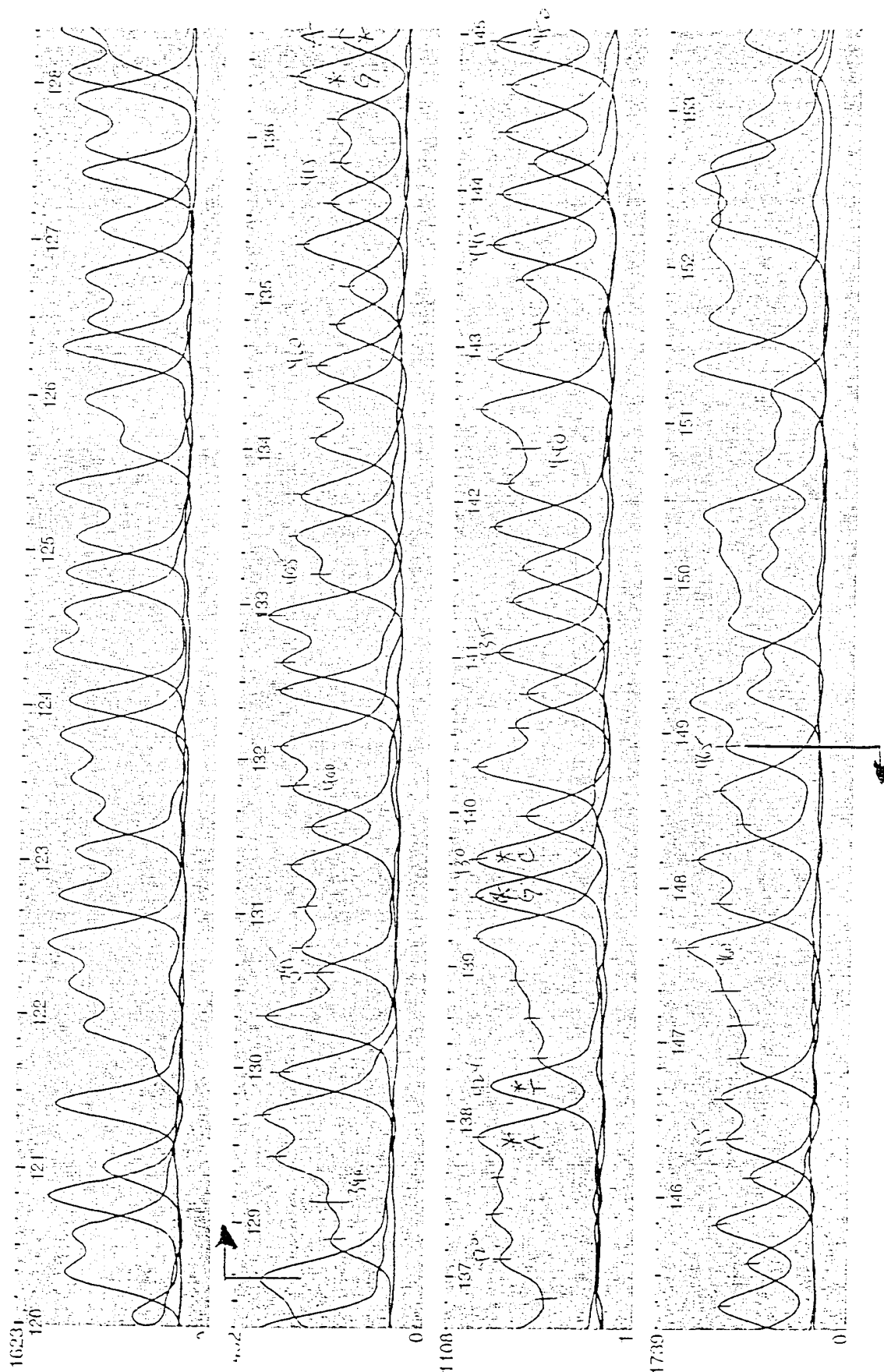
Deviation of the peak position (in number of bases) from the average
as a function of base number in different traces before alignment

Base number, nt

Deviation from the average, nt

Series1
Series2
Series3
Series4
Series5
Series6
Series7
Series8
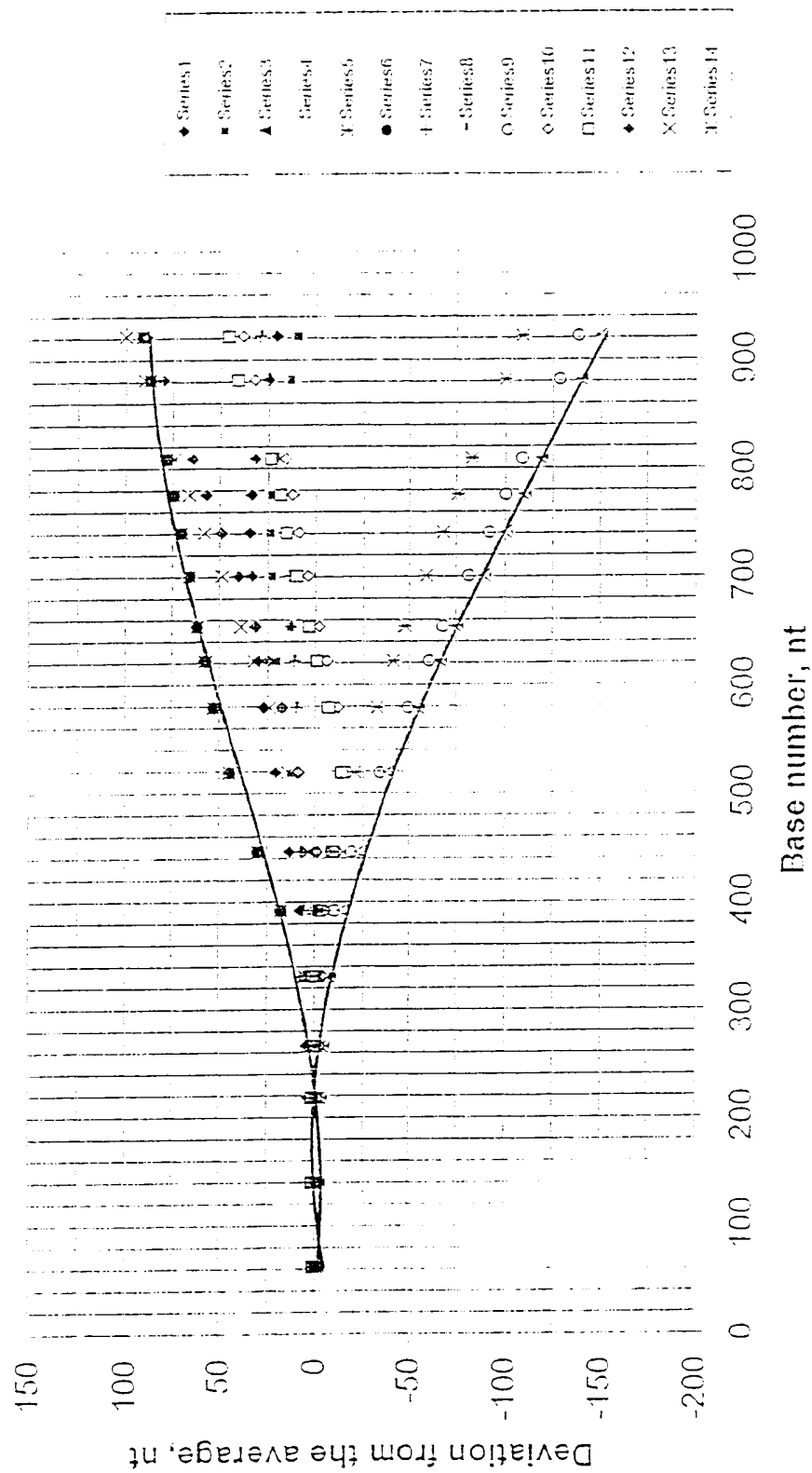Series9
Series10
Series11
Series12
Series13
Series14

Figure 10

Deviation of the peak position (in number of bases) from the average as a function of base number in the traces aligned with internal standards
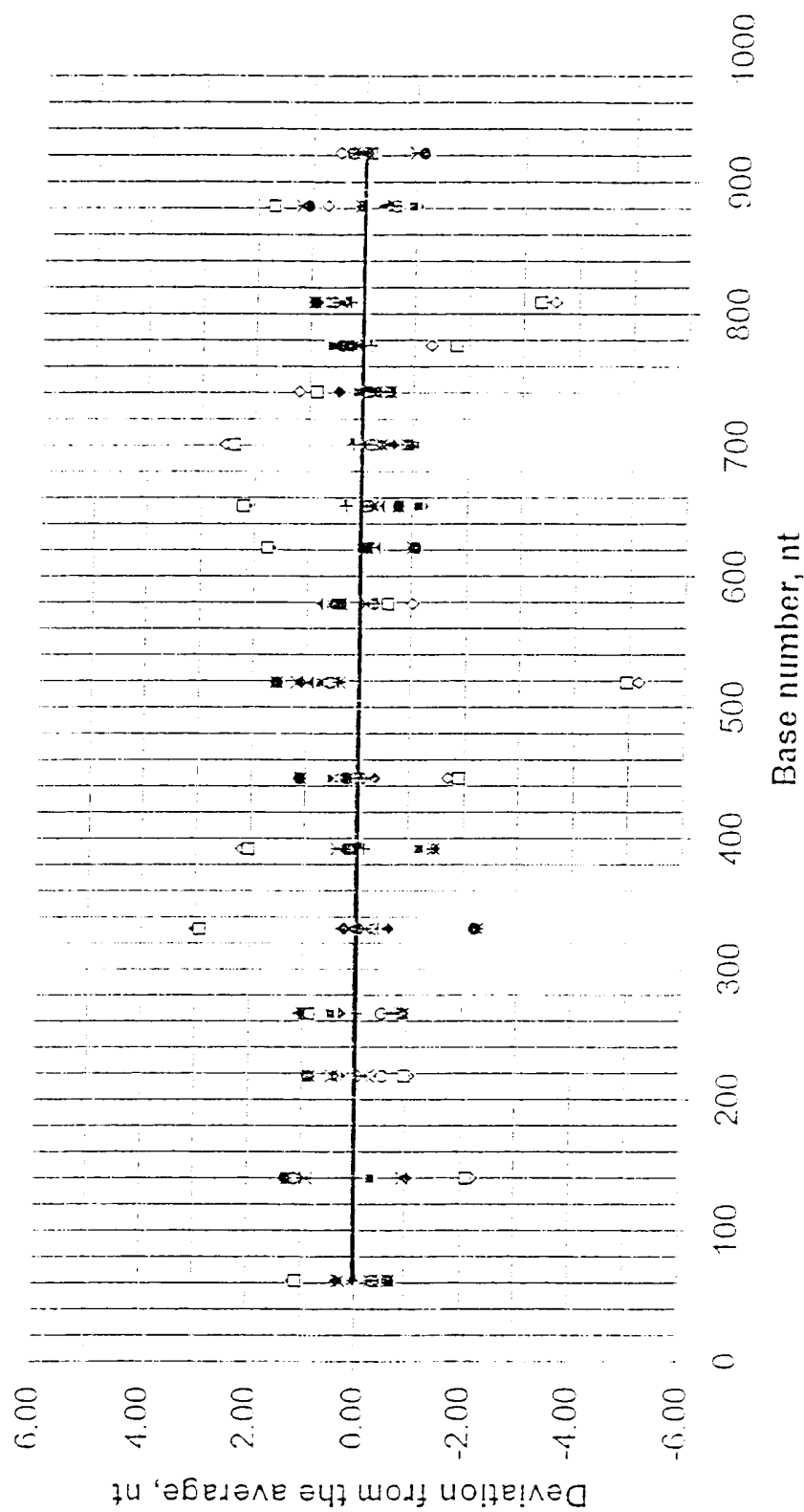
(long gel, M13, 5-th degree polynomial) 17 ref. peaks

Figure 11

Deviation of the peak position from the average as a function of base number in the traces aligned with internal standards (long gel, M13, 6 peaks, 5-th degree polynomial)
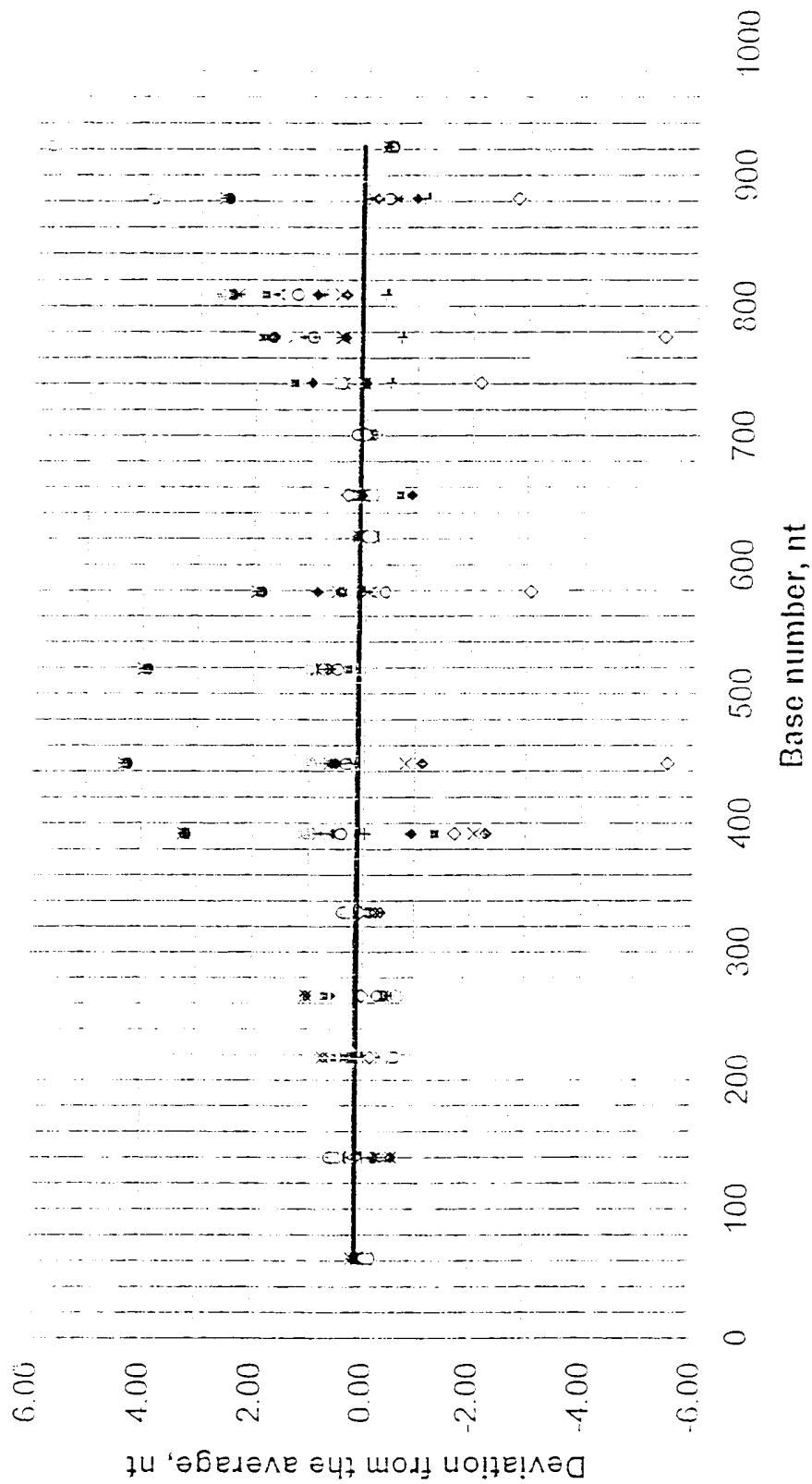
Figure 12